

DS 621 Fall2020: Homework 5 (Group3)

Wine Regression

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Overview

The wine dataset is a highly popular one in the data science community, as it models some of the challenges of real world datasets and can be modeled by a variety of different model types.

We will first explore the data looking for issues or challenges (i.e. missing data, outliers, possible coding errors, multicollinearity, etc). Once we have a handle on the data, we will apply any necessary cleaning steps. Once we have a reasonable dataset to work with, we will build and evaluate three different linear models that predict sales. Our dataset includes both training data and evaluation data - we will train using the main training data, then evaluate models based on how well they perform against the holdout evaluation data. Finally we will select a final model that offers the best compromise between accuracy and simplicity.

1. Data Exploration

Dataset

The wine training set contains 16 columns - including the target variable TARGET - and 12795 rows, covering a variety of different brands of wine. The data-set is entirely numerical variables, but also contains some variables that are highly discrete and have a limited number of possible values. We believe it is still reasonable to treat these as numerical variables since the different values follow a natural numerical order.

Below, we created a chart that describes each variable in the dataset and the theoretical effect it will have on the number of wins projected for a team.

VARIABLE NAME	DEFINITION	THEORETICAL EFFECT
INDEX	Identification Variable (do not use)	None
TARGET	Number of Cases Purchased	None
AcidIndex	Proprietary method of testing total acidity of wine by using a weighted average	
Alcohol	Alcohol Content	
Chlorides	Chloride content of wine	
CitricAcid	Citric Acid Content	
Density	Density of Wine	
FixedAcidity	Fixed Acidity of Wine	
FreeSulfurDioxide	Sulfur Dioxide content of wine	
LabelAppeal	Marketing Score indicating the appeal of label design for consumers. High numbers suggest customers like the label design. Negative numbers suggest customers don't like the design.	Many consumers purchase based on the visual appeal of the wine label design. Higher numbers suggest better sales.
ResidualSugar	Residual Sugar of wine	
STARS	Wine rating by a team of experts. 4 Stars = Excellent, 1 Star = Poor	A high number of stars suggests high sales
Sulphates	Sulfate content of wine	
TotalSulfurDioxide	Total Sulfur Dioxide of Wine	
VolatileAcidity	Volatile Acid content of wine	
pH	pH of wine	

Figure 1: Variables of Interest

Given that the Index column had no impact on the target variable, number of wines, it was dropped.

Summary Stats

We compiled summary statistics on our data set to better understand the data before modeling.

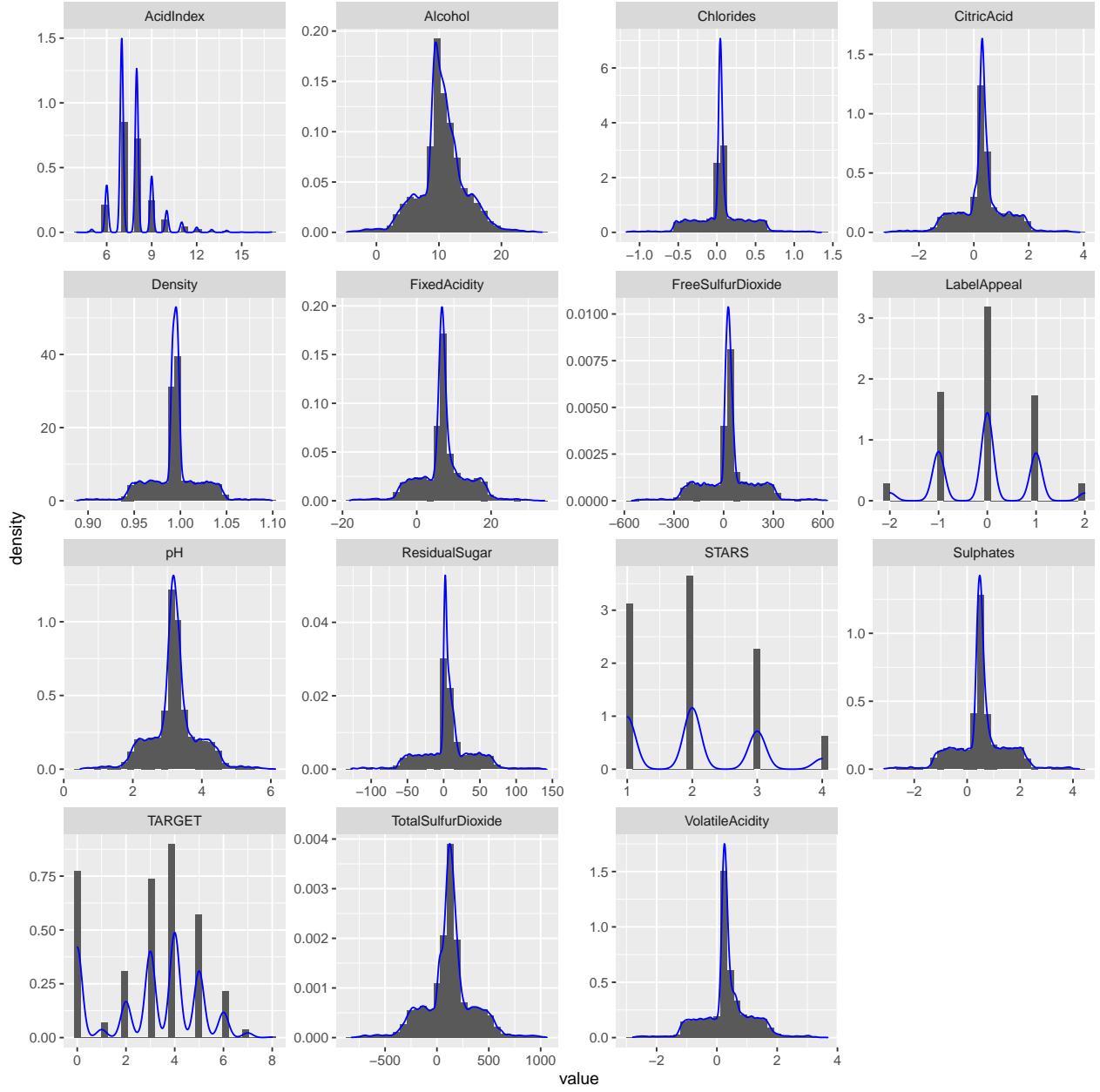
```
##      TARGET      FixedAcidity      VolatileAcidity      CitricAcid
##  Min.   :0.000   Min.   :-18.100   Min.   :-2.7900   Min.   :-3.2400
##  1st Qu.:2.000   1st Qu.: 5.200   1st Qu.: 0.1300   1st Qu.: 0.0300
##  Median :3.000   Median : 6.900   Median : 0.2800   Median : 0.3100
##  Mean   :3.029   Mean   : 7.076   Mean   : 0.3241   Mean   : 0.3084
##  3rd Qu.:4.000   3rd Qu.: 9.500   3rd Qu.: 0.6400   3rd Qu.: 0.5800
##  Max.   :8.000   Max.   :34.400   Max.   : 3.6800   Max.   : 3.8600
##
##      ResidualSugar      Chlorides      FreeSulfurDioxide TotalSulfurDioxide
##  Min.   :-127.800   Min.   :-1.1710   Min.   :-555.00   Min.   :-823.0
##  1st Qu.: -2.000   1st Qu.: -0.0310   1st Qu.:  0.00   1st Qu.:  27.0
##  Median :  3.900   Median :  0.0460   Median :  30.00   Median : 123.0
##  Mean   :  5.419   Mean   :  0.0548   Mean   :  30.85   Mean   : 120.7
##  3rd Qu.: 15.900   3rd Qu.: 0.1530   3rd Qu.:  70.00   3rd Qu.: 208.0
##  Max.   : 141.150  Max.   : 1.3510   Max.   : 623.00   Max.   :1057.0
##  NA's   :616       NA's   :638      NA's   :647      NA's   :682
##      Density          pH      Sulphates      Alcohol
##  Min.   :0.8881   Min.   :0.480   Min.   :-3.1300   Min.   :-4.70
##  1st Qu.:0.9877   1st Qu.:2.960   1st Qu.: 0.2800   1st Qu.: 9.00
##  Median :0.9945   Median :3.200   Median : 0.5000   Median :10.40
##  Mean   :0.9942   Mean   :3.208   Mean   : 0.5271   Mean   :10.49
##  3rd Qu.:1.0005   3rd Qu.:3.470   3rd Qu.: 0.8600   3rd Qu.:12.40
##  Max.   :1.0992   Max.   :6.130   Max.   : 4.2400   Max.   :26.50
##  NA's   :395       NA's   :1210    NA's   :1210    NA's   :653
##      LabelAppeal      AcidIndex      STARS
##  Min.   :-2.000000   Min.   : 4.000   Min.   :1.000
##  1st Qu.: -1.000000  1st Qu.: 7.000   1st Qu.:1.000
##  Median : 0.000000   Median : 8.000   Median :2.000
##  Mean   : -0.009066  Mean   : 7.773   Mean   :2.042
##  3rd Qu.: 1.000000   3rd Qu.: 8.000   3rd Qu.:3.000
##  Max.   : 2.000000   Max.   :17.000   Max.   :4.000
##  NA's   :3359
```

The first observation is the prevalence of NA's throughout the dataset. Of the 14 feature columns, 8 of them contain at least some NA values. We also see that the TARGET value is always between 0 and 8, which makes sense as this is the “Number of Cases of Wine Sold” (we would not expect partial cases).

We also note that many of the numerical features measuring the quantity of a chemical in the wine have a negative minimum value. We are assuming the original chemical measurements were normalized (possibly a log transform) allowing for negative values, since technically negative concentrations shouldn't be physically possible. As such, we chose to leave those values as-is.

Distributions

Next, we wanted to get an idea of the distribution profiles for each of the variables.



We see that most variables have a somewhat normal (although steep) distribution.

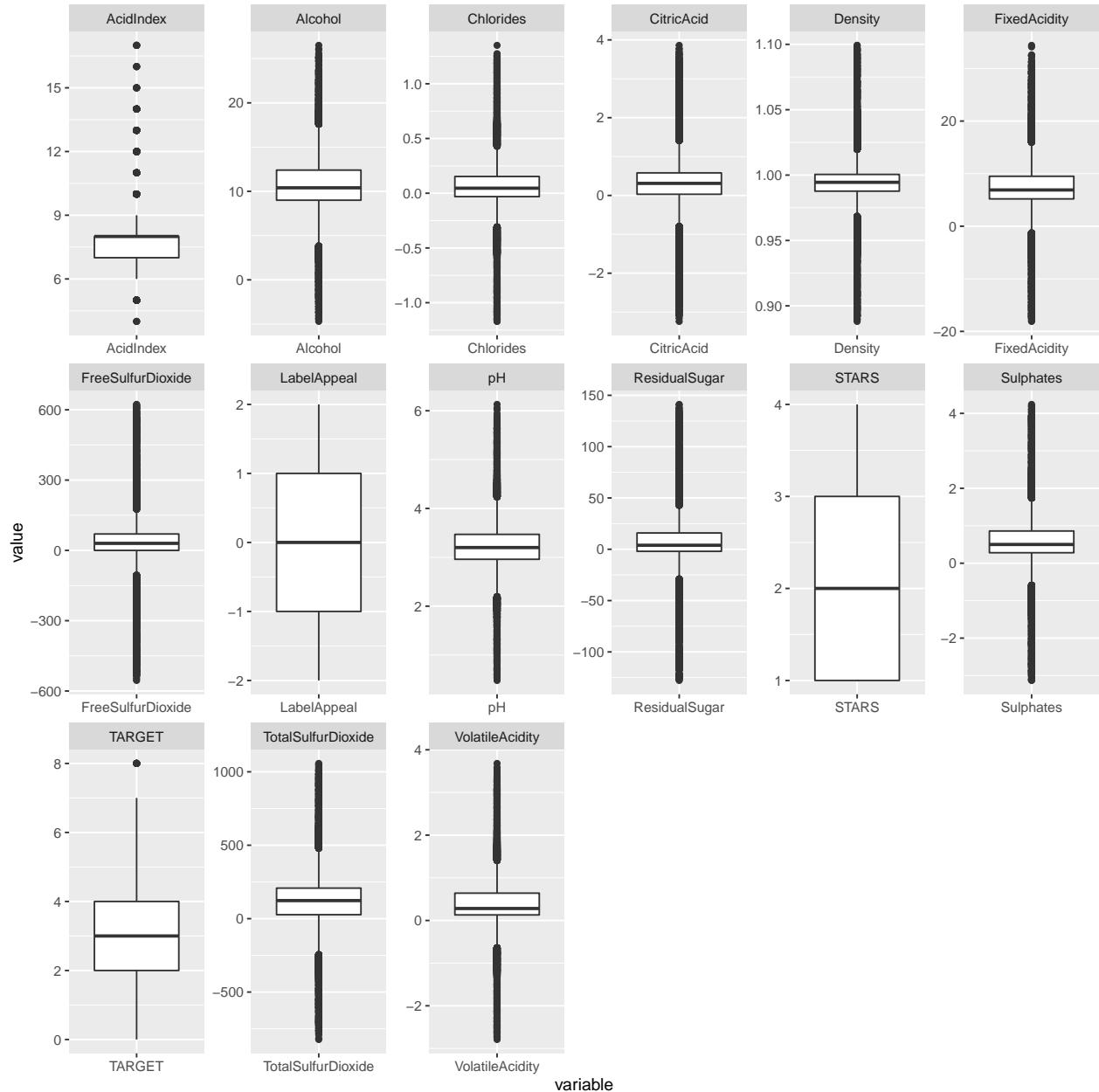
The distribution profiles show right skew in variables `AcidIndex`, and `STARS`.

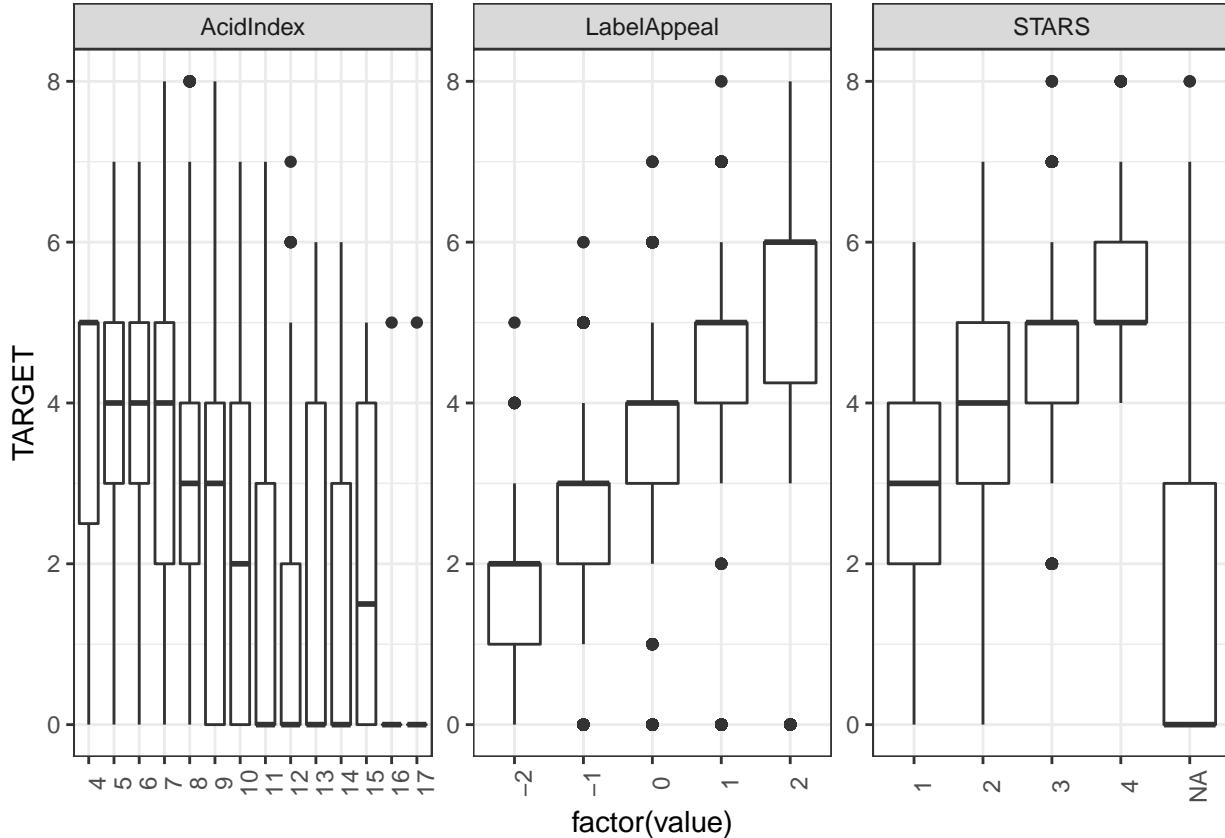
More interesting is the shape of many features where they are centered with most values clustered at the center and somewhat uniform shape above and below. It almost appears like a tri-modal distribution with a low, middle and high normal distributions overlapping. We are not going to do extensive feature engineering, or we might consider breaking these features up into 3 separate features each. Two approaches include:

1. Use `mixTools` to separate the multi-modal curves into 3 distinct (and separate) features each capturing just the `low`, `middle` or `high` values and retaining a numerical value.
2. Discretize the features converting them into categorical values indicating `low`, `middle` or `high` value.

Boxplots

In addition to creating histogram distributions, we also elected to use box-plots to get an idea of the spread of each variable.



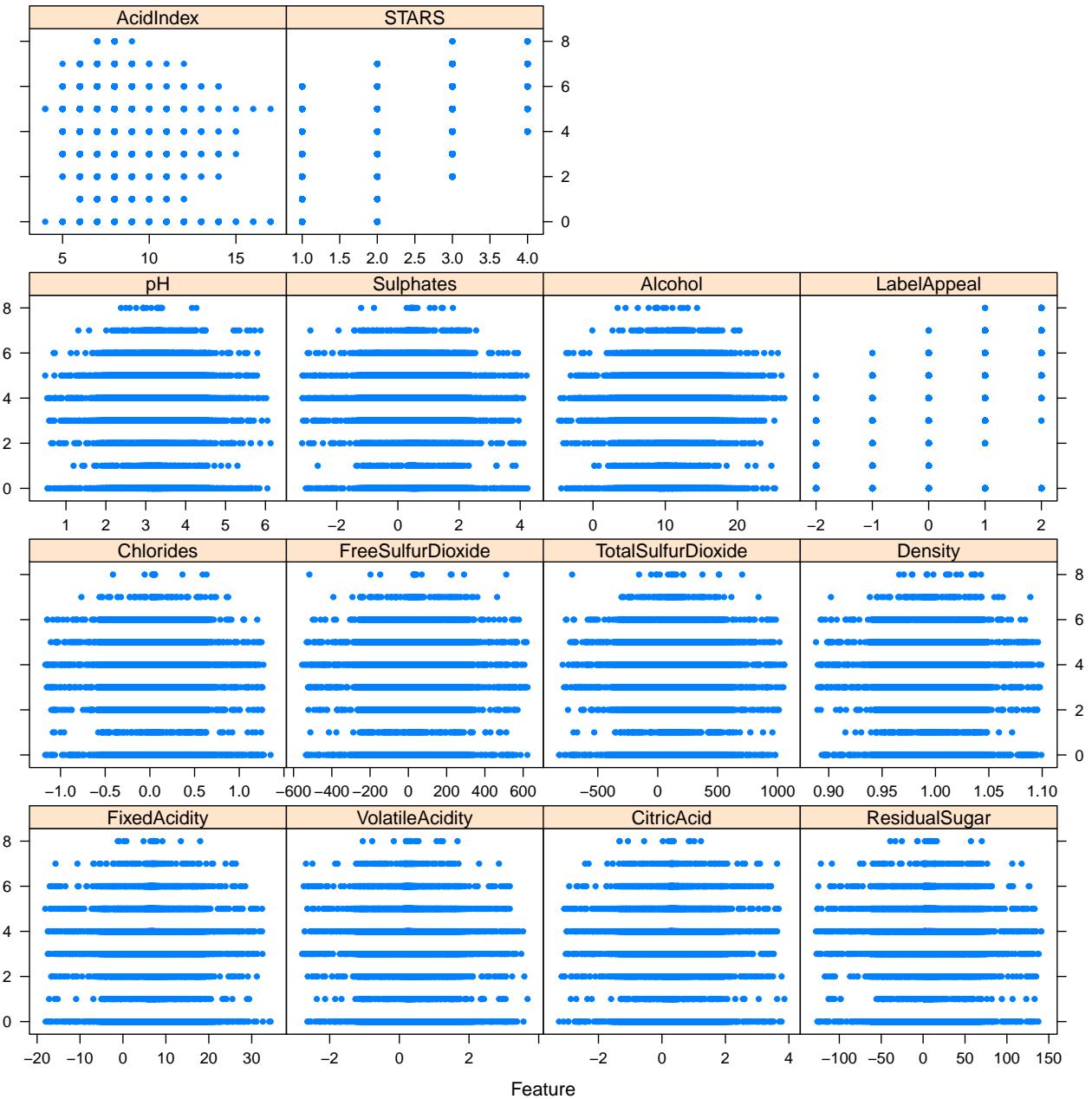


The box-plots do not reveal any enormous outliers in any of the features, meaning it is unlikely we will need to perform outlier detection and removal. **AcidIndex**, **LabelAppeal**, and **STARS** are essentially categorical in nature (ordinal), so we explore how each value of those features relates with **TARGET**. We see a clear relationship - as **LabelAppeal** increases, so does **TARGET**.

We see the same relationship between **STARS** and **TARGET** - we especially note that **STARS=NA** highly correlates with lower **TARGET**. In the original project instructions, attention was drawn to the fact that missing data might be informative. Based on this, we will impute **STARS=NA** into **STARS=0** which fits with the other values we see for **STARS** and the pattern that as stars increase, cases sold increase.

Variable Plots

Finally, we wanted to plot scatter plots of each variable versus the target variable, **TARGET**, to get an idea of the relationship between them.



Due to the discrete nature of the target, it is somewhat difficult to see clear linear relationships in the data. However, it does appear that both **STARS** and **LabelAppeal** have a significant positive relationship with the TARGET, and many of the chemical features have at least some negative relationship with the TARGET as lower values led to more values of 8 and 7 in the target variable.

Overall, although our plots indicate some interesting relationships between our variables, they also reveal some significant issues with the data.

For instance, there are many data points that contain missing data that will need to be either imputed or discarded. There also was the issue of nonsensical negative values for variables measuring a concentration; we have chosen to assume that these variables have been log transformed and these values are not in error. However, there is no evidence to back up this decision, and we would need to reevaluate if given more information on the data collection/transformation process.

Missing Data

When we initially viewed the first few rows of the raw data, we already noticed missing data. Let's assess which fields have missing data.

```
##      values          ind
## 1    26.25        STARS
## 2     9.46        Sulphates
## 3    5.33 TotalSulfurDioxide
## 4    5.10        Alcohol
## 5    5.06 FreeSulfurDioxide
## 6    4.99        Chlorides
## 7    4.81 ResidualSugar
## 8    3.09          pH
## 9    0.00        TARGET
## 10   0.00 FixedAcidity
## 11   0.00 VolatileAcidity
## 12   0.00        CitricAcid
## 13   0.00          Density
## 14   0.00 LabelAppeal
## 15   0.00 AcidIndex
```

In the project description, it was noted that the fact that a certain variable is missing may be predictive. We will impute `STARS=NA` to `STARS=0`. We will impute the remaining missing data using `caret::preProcess` and `method=knnImpute`. Note that `preProcess` will also center, scale and BoxCox our features at the same time.

Feature-Target Correlations

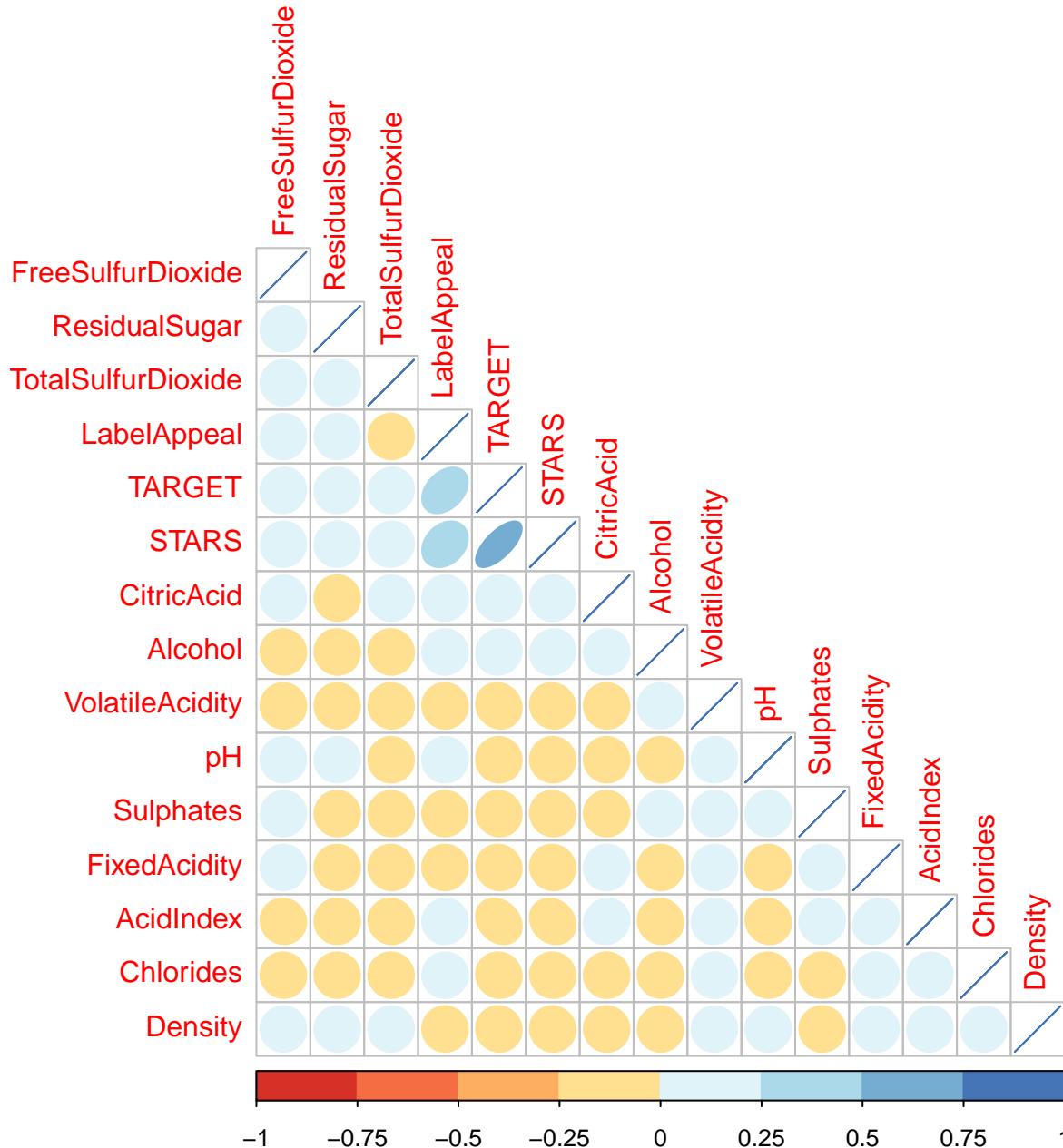
With our missing data imputed correctly, we can now build off the scatter plots from above to quantify the correlations between our target variable and predictor variable. We will want to choose those with stronger positive or negative correlations. Features with correlations closer to zero will probably not provide any meaningful information on explaining wins by a team.

```
##      values          ind
## 1    0.685381473        STARS
## 2    0.356500469 LabelAppeal
## 3    0.062030498        Alcohol
## 4    0.051730323 TotalSulfurDioxide
## 5    0.043996542 FreeSulfurDioxide
## 6    0.016187709 ResidualSugar
## 7    0.008684633        CitricAcid
## 8   -0.009081197          pH
## 9   -0.035589560          Density
## 10   -0.039072231        Chlorides
## 11   -0.039917146        Sulphates
## 12   -0.049010939 FixedAcidity
## 13   -0.088793212 VolatileAcidity
## 14   -0.221991949 AcidIndex
```

`STARS`, `LabelAppeal`, and `AcidIndex` have the highest correlation with `TARGET`, which matches what we saw in the variable plots above. Recall that we imputed `NA` values for `STARS` as 0.

Multicollinearity

One problem that can occur with multi-variable regression is correlation between variables, or multicollinearity. A quick check is to run correlations between variables.



We see that the features have very low correlations with each other, meaning that there is not much multicollinearity present in the dataset. This means that the assumptions of linear regression are more likely to be met.

2. Data Preparation

To summarize our data preparation and exploration, we can distinguish our findings into a few categories below:

Removed Fields

We removed the INDEX field as it offers no information for a model.

Missing Values

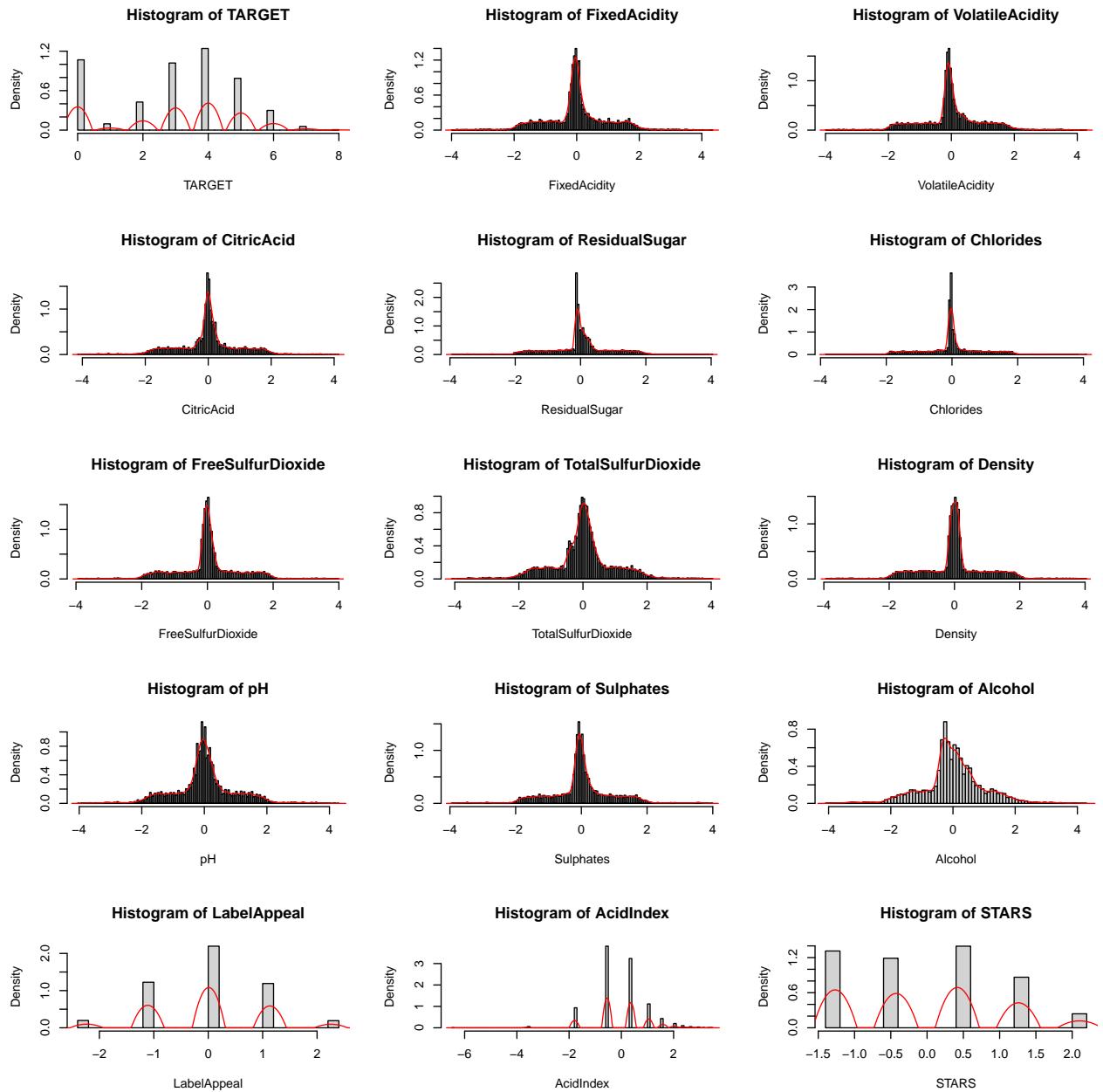
For the STARS field, we imputed NAs as the value of 0, since missing values were highly correlated with the target variable. For other fields with missing values, we imputed their value using caret's knnimpute.

Outliers

Many of the numerical features have somewhat unreasonable negative values, but we are choosing to believe that these are log-transformed variables and that the values are legitimate.

Transform non-normal variables

Finally, as mentioned earlier in our data exploration, during the impute step, `caret::preProcess()` automatically centered, scaled and BoxCox transformed our data. Here are some plots to demonstrate the changes in distributions and final values after the transformations:



We see that after the transformations, the variables are more centered and more closely resemble a normal distribution, although clearly they are still not perfect normal distributions.

Finalizing the dataset for model building

With our transformations complete, we can now add these into our `clean_df` data frame and continue on to build our models. To better measure each model performance, we split our data into a training and testing data set. We will train using the first, then measure model performance again the testing hold out set.

```
## [1] "Number of Training Samples: 10238"
```

```
## [1] "Number of Testing Samples: 2557"
```

3. Model Building

Poisson Model 1

In this first model, we include all available features. Features include:

FixedAcidity, VolatileAcidity, CitricAcid, ResidualSugar, Chlorides, FreeSulfurDioxide, TotalSulfurDioxide, Density, pH, Sulphates, Alcohol, LabelAppeal, AcidIndex, STARS

```
##  
## Call:  
## glm(formula = TARGET ~ FixedAcidity + VolatileAcidity + CitricAcid +  
##       ResidualSugar + Chlorides + FreeSulfurDioxide + TotalSulfurDioxide +  
##       Density + pH + Sulphates + Alcohol + as.factor(LabelAppeal) +  
##       as.factor(AcidIndex) + as.factor(STARS), family = poisson,  
##       data = trainingData)  
##  
## Deviance Residuals:  
##      Min        1Q     Median        3Q       Max  
## -3.2346   -0.6292   -0.0082    0.4352   3.7115  
##  
## Coefficients:  
##                                     Estimate Std. Error z value  
## (Intercept)                   1.0451474  0.4493999  2.326  
## FixedAcidity                  0.0039350  0.0058308  0.675  
## VolatileAcidity                -0.0236702 0.0056895 -4.160  
## CitricAcid                     0.0030649  0.0056881  0.539  
## ResidualSugar                 -0.0002512 0.0058111 -0.043  
## Chlorides                      -0.0131661 0.0058269 -2.260  
## FreeSulfurDioxide               0.0149673  0.0058427  2.562  
## TotalSulfurDioxide              0.0150621  0.0058624  2.569  
## Density                        -0.0119753 0.0056984 -2.102  
## pH                             -0.0054008 0.0058036 -0.931  
## Sulphates                      -0.0120172 0.0059479 -2.020  
## Alcohol                         0.0151180  0.0058460  2.586  
## as.factor(LabelAppeal)-1.11204793733397 0.2344060  0.0411662  5.694  
## as.factor(LabelAppeal)0.0101741115806247 0.4236828  0.0400792 10.571  
## as.factor(LabelAppeal)1.13239616049522 0.5555679  0.0408132 13.612  
## as.factor(LabelAppeal)2.25461820940981 0.6900548  0.0463427 14.890  
## as.factor(AcidIndex)-3.59682937695875 -1.1812180 0.4528622 -2.608  
## as.factor(AcidIndex)-1.79176983045029 -1.1505324 0.4483228 -2.566  
## as.factor(AcidIndex)-0.545318540973785 -1.1728280 0.4480808 -2.617  
## as.factor(AcidIndex)0.362910765511677 -1.2102925 0.4481148 -2.701  
## as.factor(AcidIndex)1.05172974217783 -1.3052019 0.4483606 -2.911  
## as.factor(AcidIndex)1.59059728918163 -1.4681077 0.4492942 -3.268  
## as.factor(AcidIndex)2.02271372429848 -1.8482159 0.4523108 -4.086  
## as.factor(AcidIndex)2.37629509167962 -1.7963493 0.4568280 -3.932  
## as.factor(AcidIndex)2.67051656830802 -1.6115734 0.4594526 -3.508  
## as.factor(AcidIndex)2.9188445277671 -1.5961513 0.4668320 -3.419  
## as.factor(AcidIndex)3.13100139587667 -1.3439213 0.5329855 -2.521  
## as.factor(AcidIndex)3.31417429494859 -13.8251887 164.0941075 -0.084  
## as.factor(AcidIndex)3.47378568897179 -1.9897846 0.6333123 -3.142  
## as.factor(STARS)-0.42623524866846 0.7654253 0.0219835 34.818  
## as.factor(STARS)0.416552574962037 1.0838390 0.0204856 52.907
```

```

## as.factor(STARS)1.25934039859254      1.1978217  0.0216009 55.452
## as.factor(STARS)2.10212822222303      1.3254179  0.0274024 48.369
##
## (Intercept)                                Pr(>|z|)
## FixedAcidity                               0.020037 *
## VolatileAcidity                            0.499762
## CitricAcid                                 0.0000317774 ***
## ResidualSugar                              0.590013
## Chlorides                                   0.965516
## FreeSulfurDioxide                          0.023850 *
## TotalSulfurDioxide                         0.010416 *
## Density                                     0.010191 *
## pH                                         0.035596 *
## Sulphates                                   0.352062
## Alcohol                                    0.043339 *
##                                         0.009708 **
## as.factor(LabelAppeal)-1.11204793733397    0.0000000124 ***
## as.factor(LabelAppeal)0.0101741115806247 < 0.0000000000000002 ***
## as.factor(LabelAppeal)1.13239616049522 < 0.0000000000000002 ***
## as.factor(LabelAppeal)2.25461820940981 < 0.0000000000000002 ***
## as.factor(AcidIndex)-3.59682937695875     0.009098 **
## as.factor(AcidIndex)-1.79176983045029     0.010279 *
## as.factor(AcidIndex)-0.545318540973785    0.008859 **
## as.factor(AcidIndex)0.362910765511677     0.006916 **
## as.factor(AcidIndex)1.05172974217783     0.003602 **
## as.factor(AcidIndex)1.59059728918163     0.001085 **
## as.factor(AcidIndex)2.02271372429848     0.0000438564 ***
## as.factor(AcidIndex)2.37629509167962     0.0000841640 ***
## as.factor(AcidIndex)2.67051656830802     0.000452 ***
## as.factor(AcidIndex)2.9188445277671     0.000628 ***
## as.factor(AcidIndex)3.13100139587667     0.011686 *
## as.factor(AcidIndex)3.31417429494859     0.932856
## as.factor(AcidIndex)3.47378568897179     0.001679 **
## as.factor(STARS)-0.42623524866846     < 0.0000000000000002 ***
## as.factor(STARS)0.416552574962037     < 0.0000000000000002 ***
## as.factor(STARS)1.25934039859254      < 0.0000000000000002 ***
## as.factor(STARS)2.10212822222303      < 0.0000000000000002 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
## Null deviance: 18090  on 10237  degrees of freedom
## Residual deviance: 10639  on 10205  degrees of freedom
## AIC: 36337
##
## Number of Fisher Scoring iterations: 10

##          RMSE       Rsquared        MAE        aic        bic
##      2.5921891   0.4659337   2.2257186 36337.4276366 36576.1450683

```

Poisson Model 2

In this second model, we only include the most predictive features based on our first Poisson Model. The predictors for the following model are:

VolatileAcidity, TotalSulfurDioxide, Alcohol, LabelAppeal, AcidIndex, STARS

```
##
## Call:
## glm(formula = TARGET ~ VolatileAcidity + TotalSulfurDioxide +
##       Alcohol + as.factor(LabelAppeal) + as.factor(AcidIndex) +
##       as.factor(STARS), family = poisson, data = clean_df)
##
## Deviance Residuals:
##    Min      1Q   Median      3Q     Max 
## -3.2335 -0.6501 -0.0035  0.4410  3.6951 
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                0.001201  0.318675  0.004
## VolatileAcidity            -0.023533  0.005122 -4.595
## TotalSulfurDioxide          0.016952  0.005244  3.232
## Alcohol                     0.016009  0.005231  3.060
## as.factor(LabelAppeal)-1.11204793733397  0.240289  0.037999  6.324
## as.factor(LabelAppeal)0.0101741115806247  0.430806  0.037064 11.623
## as.factor(LabelAppeal)1.13239616049522  0.564104  0.037710 14.959
## as.factor(LabelAppeal)2.25461820940981  0.699216  0.042446 16.473
## as.factor(AcidIndex)-3.59682937695875  -0.140143  0.322337 -0.435
## as.factor(AcidIndex)-1.79176983045029  -0.097789  0.316887 -0.309
## as.factor(AcidIndex)-0.545318540973785  -0.131342  0.316605 -0.415
## as.factor(AcidIndex)0.362910765511677  -0.162635  0.316637 -0.514
## as.factor(AcidIndex)1.05172974217783  -0.272917  0.316940 -0.861
## as.factor(AcidIndex)1.59059728918163  -0.432064  0.318025 -1.359
## as.factor(AcidIndex)2.02271372429848  -0.795786  0.321596 -2.474
## as.factor(AcidIndex)2.37629509167962  -0.810861  0.327262 -2.478
## as.factor(AcidIndex)2.67051656830802  -0.646459  0.330156 -1.958
## as.factor(AcidIndex)2.9188445277671  -0.738613  0.342710 -2.155
## as.factor(AcidIndex)3.13100139587667  -0.286638  0.403433 -0.710
## as.factor(AcidIndex)3.31417429494859  -0.951704  0.547993 -1.737
## as.factor(AcidIndex)3.47378568897179  -1.196936  0.548071 -2.184
## as.factor(STARS)-0.42623524866846  0.757245  0.019564 38.705
## as.factor(STARS)0.416552574962037  1.075518  0.018261 58.896
## as.factor(STARS)1.25934039859254  1.194174  0.019232 62.093
## as.factor(STARS)2.10212822222303  1.313789  0.024330 53.999
##
##                               Pr(>|z|)
## (Intercept)                0.99699
## VolatileAcidity            0.000004335408 ***
## TotalSulfurDioxide          0.00123 **
## Alcohol                     0.00221 **
## as.factor(LabelAppeal)-1.11204793733397  0.000000000256 ***
## as.factor(LabelAppeal)0.0101741115806247 < 0.0000000000000002 ***
## as.factor(LabelAppeal)1.13239616049522  < 0.0000000000000002 ***
## as.factor(LabelAppeal)2.25461820940981  < 0.0000000000000002 ***
## as.factor(AcidIndex)-3.59682937695875  0.66373
## as.factor(AcidIndex)-1.79176983045029  0.75763
## as.factor(AcidIndex)-0.545318540973785  0.67825
## as.factor(AcidIndex)0.362910765511677  0.60751
## as.factor(AcidIndex)1.05172974217783  0.38918
## as.factor(AcidIndex)1.59059728918163  0.17428
```

```

## as.factor(AcidIndex)2.02271372429848          0.01334 *
## as.factor(AcidIndex)2.37629509167962          0.01322 *
## as.factor(AcidIndex)2.67051656830802          0.05023 .
## as.factor(AcidIndex)2.9188445277671          0.03114 *
## as.factor(AcidIndex)3.13100139587667          0.47740
## as.factor(AcidIndex)3.31417429494859          0.08244 .
## as.factor(AcidIndex)3.47378568897179          0.02897 *
## as.factor(STARS)-0.42623524866846 < 0.0000000000000002 ***
## as.factor(STARS)0.416552574962037 < 0.0000000000000002 ***
## as.factor(STARS)1.25934039859254 < 0.0000000000000002 ***
## as.factor(STARS)2.10212822222303 < 0.0000000000000002 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
## Null deviance: 22861 on 12794 degrees of freedom
## Residual deviance: 13550 on 12770 degrees of freedom
## AIC: 45542
##
## Number of Fisher Scoring iterations: 6

##           RMSE      Rsquared       MAE        aic        bic
##     2.5850440    0.5228423   2.2246205 45542.3183589 45728.7386026

```

Negative Binomial Model 3

Similar to Poisson Model 1, the predictors for the following model are:

FixedAcidity, VolatileAcidity, CitricAcid, ResidualSugar, Chlorides, FreeSulfurDioxide, TotalSulfurDioxide, Density, pH, Sulphates, Alcohol, LabelAppeal, AcidIndex, STARS

```

##
## Call:
## glm.nb(formula = TARGET ~ FixedAcidity + VolatileAcidity + CitricAcid +
##         ResidualSugar + Chlorides + FreeSulfurDioxide + TotalSulfurDioxide +
##         Density + pH + Sulphates + Alcohol + as.factor(LabelAppeal) +
##         as.factor(AcidIndex) + as.factor(STARS), data = clean_df,
##         init.theta = 40957.00204, link = log)
##
## Deviance Residuals:
##       Min      1Q      Median      3Q      Max
## -3.2219 -0.6496 -0.0055  0.4446  3.6790
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                 0.0275198  0.3190721  0.086
## FixedAcidity                0.0010176  0.0051829  0.196
## VolatileAcidity             -0.0231944  0.0051231 -4.527
## CitricAcid                  0.0039724  0.0050838  0.781
## ResidualSugar               0.0005767  0.0052060  0.111
## Chlorides                   -0.0122552  0.0052206 -2.347
## FreeSulfurDioxide            0.0132531  0.0051832  2.557

```

## TotalSulfurDioxide	0.0170166	0.0052484	3.242
## Density	-0.0074549	0.0050938	-1.464
## pH	-0.0066655	0.0051875	-1.285
## Sulphates	-0.0106282	0.0053149	-2.000
## Alcohol	0.0157805	0.0052355	3.014
## as.factor(LabelAppeal)-1.11204793733397	0.2398534	0.0380017	6.312
## as.factor(LabelAppeal)0.0101741115806247	0.4300463	0.0370666	11.602
## as.factor(LabelAppeal)1.13239616049522	0.5633460	0.0377142	14.937
## as.factor(LabelAppeal)2.25461820940981	0.6992610	0.0424548	16.471
## as.factor(AcidIndex)-3.59682937695875	-0.1651538	0.3226593	-0.512
## as.factor(AcidIndex)-1.79176983045029	-0.1214774	0.3172467	-0.383
## as.factor(AcidIndex)-0.545318540973785	-0.1558113	0.3169954	-0.492
## as.factor(AcidIndex)0.362910765511677	-0.1871144	0.3170413	-0.590
## as.factor(AcidIndex)1.05172974217783	-0.2972766	0.3173791	-0.937
## as.factor(AcidIndex)1.59059728918163	-0.4542592	0.3184811	-1.426
## as.factor(AcidIndex)2.02271372429848	-0.8158352	0.3220684	-2.533
## as.factor(AcidIndex)2.37629509167962	-0.8303961	0.3277299	-2.534
## as.factor(AcidIndex)2.67051656830802	-0.6688133	0.3306330	-2.023
## as.factor(AcidIndex)2.9188445277671	-0.7687131	0.3432641	-2.239
## as.factor(AcidIndex)3.13100139587667	-0.3297889	0.4038365	-0.817
## as.factor(AcidIndex)3.31417429494859	-0.9814037	0.5484760	-1.789
## as.factor(AcidIndex)3.47378568897179	-1.2022430	0.5486104	-2.191
## as.factor(STARS)-0.42623524866846	0.7548590	0.0195728	38.567
## as.factor(STARS)0.416552574962037	1.0732229	0.0182738	58.730
## as.factor(STARS)1.25934039859254	1.1910222	0.0192473	61.880
## as.factor(STARS)2.10212822222303	1.3117031	0.0243440	53.882
##		Pr(> z)	
## (Intercept)		0.93127	
## FixedAcidity		0.84435	
## VolatileAcidity		0.000005971523 ***	
## CitricAcid		0.43458	
## ResidualSugar		0.91179	
## Chlorides		0.01890 *	
## FreeSulfurDioxide		0.01056 *	
## TotalSulfurDioxide		0.00119 **	
## Density		0.14332	
## pH		0.19882	
## Sulphates		0.04554 *	
## Alcohol		0.00258 **	
## as.factor(LabelAppeal)-1.11204793733397		0.000000000276 ***	
## as.factor(LabelAppeal)0.0101741115806247	<	0.0000000000000002 ***	
## as.factor(LabelAppeal)1.13239616049522	<	0.0000000000000002 ***	
## as.factor(LabelAppeal)2.25461820940981	<	0.0000000000000002 ***	
## as.factor(AcidIndex)-3.59682937695875		0.60875	
## as.factor(AcidIndex)-1.79176983045029		0.70179	
## as.factor(AcidIndex)-0.545318540973785		0.62305	
## as.factor(AcidIndex)0.362910765511677		0.55506	
## as.factor(AcidIndex)1.05172974217783		0.34893	
## as.factor(AcidIndex)1.59059728918163		0.15377	
## as.factor(AcidIndex)2.02271372429848		0.01131 *	
## as.factor(AcidIndex)2.37629509167962		0.01128 *	
## as.factor(AcidIndex)2.67051656830802		0.04309 *	
## as.factor(AcidIndex)2.9188445277671		0.02513 *	
## as.factor(AcidIndex)3.13100139587667		0.41413	

```

## as.factor(AcidIndex)3.31417429494859          0.07356 .
## as.factor(AcidIndex)3.47378568897179          0.02842 *
## as.factor(STARS)-0.42623524866846      < 0.0000000000000002 ***
## as.factor(STARS)0.416552574962037     < 0.0000000000000002 ***
## as.factor(STARS)1.25934039859254     < 0.0000000000000002 ***
## as.factor(STARS)2.10212822222303     < 0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(40957) family taken to be 1)
##
## Null deviance: 22860  on 12794  degrees of freedom
## Residual deviance: 13529  on 12762  degrees of freedom
## AIC: 45540
##
## Number of Fisher Scoring iterations: 1
##
##
##           Theta:  40957
##           Std. Err.: 34344
## Warning while fitting theta: iteration limit reached
##
## 2 x log-likelihood: -45472.13

##          RMSE      Rsquared        MAE        aic        bic
##    2.5847131    0.5244026    2.2242130 45540.1321552 45793.6636866

```

Negative Binomial Model 4

Similar to Poisson Model 2, the predictors for the following model are:

VolatileAcidity, FreeSulfurDioxide, TotalSulfurDioxide, Alcohol, LabelAppeal, AcidIndex, STARS

```

##
## Call:
## glm.nb(formula = TARGET ~ VolatileAcidity + FreeSulfurDioxide +
##         TotalSulfurDioxide + Alcohol + as.factor(LabelAppeal) + as.factor(AcidIndex) +
##         as.factor(STARS), data = clean_df, init.theta = 40912.67371,
##         link = log)
##
## Deviance Residuals:
##      Min        1Q      Median        3Q       Max
## -3.2456   -0.6517   -0.0038    0.4399    3.6952
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                  0.014317  0.318731  0.045
## VolatileAcidity              -0.023451  0.005122 -4.578
## FreeSulfurDioxide             0.013266  0.005179  2.562
## TotalSulfurDioxide            0.016879  0.005244  3.219
## Alcohol                      0.016237  0.005231  3.104
## as.factor(LabelAppeal)-1.11204793733397  0.240039  0.038000  6.317
## as.factor(LabelAppeal)0.0101741115806247  0.430314  0.037065 11.610

```

```

## as.factor(LabelAppeal)1.13239616049522      0.563287  0.037712 14.936
## as.factor(LabelAppeal)2.25461820940981      0.698162  0.042449 16.447
## as.factor(AcidIndex)-3.59682937695875      -0.154135  0.322401 -0.478
## as.factor(AcidIndex)-1.79176983045029      -0.110580  0.316945 -0.349
## as.factor(AcidIndex)-0.545318540973785      -0.143771  0.316660 -0.454
## as.factor(AcidIndex)0.362910765511677      -0.174856  0.316690 -0.552
## as.factor(AcidIndex)1.05172974217783      -0.285228  0.316994 -0.900
## as.factor(AcidIndex)1.59059728918163      -0.443142  0.318072 -1.393
## as.factor(AcidIndex)2.02271372429848      -0.806122  0.321638 -2.506
## as.factor(AcidIndex)2.37629509167962      -0.819576  0.327296 -2.504
## as.factor(AcidIndex)2.67051656830802      -0.655682  0.330193 -1.986
## as.factor(AcidIndex)2.9188445277671      -0.753474  0.342775 -2.198
## as.factor(AcidIndex)3.13100139587667      -0.299583  0.403483 -0.742
## as.factor(AcidIndex)3.31417429494859      -0.953685  0.548008 -1.740
## as.factor(AcidIndex)3.47378568897179      -1.205542  0.548094 -2.200
## as.factor(STARS)-0.42623524866846      0.756497  0.019567 38.662
## as.factor(STARS)0.416552574962037      1.074730  0.018264 58.844
## as.factor(STARS)1.25934039859254      1.193602  0.019234 62.057
## as.factor(STARS)2.10212822222303      1.314420  0.024331 54.023
##
##                                     Pr(>|z|)
## (Intercept)                      0.96417
## VolatileAcidity                  0.000004685011 ***
## FreeSulfurDioxide                 0.01042 *
## TotalSulfurDioxide                0.00129 **
## Alcohol                           0.00191 **
## as.factor(LabelAppeal)-1.11204793733397    0.000000000267 ***
## as.factor(LabelAppeal)0.0101741115806247 < 0.000000000000002 ***
## as.factor(LabelAppeal)1.13239616049522     < 0.000000000000002 ***
## as.factor(LabelAppeal)2.25461820940981     < 0.000000000000002 ***
## as.factor(AcidIndex)-3.59682937695875      0.63259
## as.factor(AcidIndex)-1.79176983045029      0.72717
## as.factor(AcidIndex)-0.545318540973785      0.64981
## as.factor(AcidIndex)0.362910765511677      0.58086
## as.factor(AcidIndex)1.05172974217783      0.36823
## as.factor(AcidIndex)1.59059728918163      0.16356
## as.factor(AcidIndex)2.02271372429848      0.01220 *
## as.factor(AcidIndex)2.37629509167962      0.01228 *
## as.factor(AcidIndex)2.67051656830802      0.04706 *
## as.factor(AcidIndex)2.9188445277671      0.02794 *
## as.factor(AcidIndex)3.13100139587667      0.45779
## as.factor(AcidIndex)3.31417429494859      0.08181 .
## as.factor(AcidIndex)3.47378568897179      0.02784 *
## as.factor(STARS)-0.42623524866846      < 0.000000000000002 ***
## as.factor(STARS)0.416552574962037      < 0.000000000000002 ***
## as.factor(STARS)1.25934039859254      < 0.000000000000002 ***
## as.factor(STARS)2.10212822222303      < 0.000000000000002 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(40912.67) family taken to be 1)
##
## Null deviance: 22860  on 12794  degrees of freedom
## Residual deviance: 13543  on 12769  degrees of freedom
## AIC: 45540

```

```

##
## Number of Fisher Scoring iterations: 1
##
##
## Theta: 40913
## Std. Err.: 34297
## Warning while fitting theta: iteration limit reached
##
## 2 x log-likelihood: -45486.18

##          RMSE      Rsquared       MAE        aic        bic
##    2.5849248    0.5233392    2.2245343 45540.1774667 45741.5113299

```

Linear Model 5

The predictors for the following model are:

FixedAcidity, VolatileAcidity, CitricAcid, ResidualSugar, Chlorides, FreeSulfurDioxide, TotalSulfurDioxide, Density, pH, Sulphates, Alcohol, LabelAppeal, AcidIndex, STARS

```

##
## Call:
## lm(formula = TARGET ~ FixedAcidity + VolatileAcidity + CitricAcid +
##     ResidualSugar + Chlorides + FreeSulfurDioxide + TotalSulfurDioxide +
##     Density + pH + Sulphates + Alcohol + as.factor(LabelAppeal) +
##     as.factor(AcidIndex) + as.factor(STARS), data = clean_df)
##
## Residuals:
##      Min      1Q  Median      3Q      Max
## -4.9635 -0.8591  0.0325  0.8384  6.0750
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                0.995095  0.755491  1.317
## FixedAcidity               0.004930  0.011720  0.421
## VolatileAcidity            -0.073667  0.011565 -6.370
## CitricAcid                 0.014455  0.011558  1.251
## ResidualSugar              0.004027  0.011782  0.342
## Chlorides                  -0.038485  0.011776 -3.268
## FreeSulfurDioxide           0.039825  0.011786  3.379
## TotalSulfurDioxide          0.049447  0.011816  4.185
## Density                    -0.022475  0.011545 -1.947
## pH                          -0.018619  0.011704 -1.591
## Sulphates                  -0.028248  0.012015 -2.351
## Alcohol                     0.050812  0.011830  4.295
## as.factor(LabelAppeal)-1.11204793733397  0.367639  0.062729  5.861
## as.factor(LabelAppeal)0.0101741115806247  0.835185  0.061168 13.654
## as.factor(LabelAppeal)1.13239616049522   1.302062  0.063917 20.371
## as.factor(LabelAppeal)2.25461820940981   1.889951  0.084169 22.454
## as.factor(AcidIndex)-3.59682937695875   -0.334854  0.767938 -0.436
## as.factor(AcidIndex)-1.79176983045029   -0.220221  0.754101 -0.292
## as.factor(AcidIndex)-0.545318540973785  -0.322349  0.753472 -0.428
## as.factor(AcidIndex)0.362910765511677   -0.429363  0.753539 -0.570

```

```

## as.factor(AcidIndex)1.05172974217783 -0.732560 0.754117 -0.971
## as.factor(AcidIndex)1.59059728918163 -1.041297 0.755385 -1.378
## as.factor(AcidIndex)2.02271372429848 -1.513113 0.757752 -1.997
## as.factor(AcidIndex)2.37629509167962 -1.533481 0.762156 -2.012
## as.factor(AcidIndex)2.67051656830802 -1.552014 0.769606 -2.017
## as.factor(AcidIndex)2.9188445277671 -1.400154 0.777299 -1.801
## as.factor(AcidIndex)3.13100139587667 -0.692206 0.883131 -0.784
## as.factor(AcidIndex)3.31417429494859 -1.772148 0.952843 -1.860
## as.factor(AcidIndex)3.47378568897179 -1.920432 0.900840 -2.132
## as.factor(STARS)-0.42623524866846 1.346560 0.032920 40.904
## as.factor(STARS)0.416552574962037 2.381720 0.032021 74.381
## as.factor(STARS)1.25934039859254 2.942287 0.037079 79.352
## as.factor(STARS)2.10212822222303 3.629958 0.059150 61.368
##
## Pr(>|t|)
## (Intercept) 0.18781
## FixedAcidity 0.67401
## VolatileAcidity 0.000000000196 ***
## CitricAcid 0.21109
## ResidualSugar 0.73251
## Chlorides 0.00109 **
## FreeSulfurDioxide 0.00073 ***
## TotalSulfurDioxide 0.000028712970 ***
## Density 0.05160 .
## pH 0.11167
## Sulphates 0.01873 *
## Alcohol 0.000017590098 ***
## as.factor(LabelAppeal)-1.11204793733397 0.000000004722 ***
## as.factor(LabelAppeal)0.0101741115806247 < 0.0000000000000002 ***
## as.factor(LabelAppeal)1.13239616049522 < 0.0000000000000002 ***
## as.factor(LabelAppeal)2.25461820940981 < 0.0000000000000002 ***
## as.factor(AcidIndex)-3.59682937695875 0.66281
## as.factor(AcidIndex)-1.79176983045029 0.77027
## as.factor(AcidIndex)-0.545318540973785 0.66879
## as.factor(AcidIndex)0.362910765511677 0.56883
## as.factor(AcidIndex)1.05172974217783 0.33136
## as.factor(AcidIndex)1.59059728918163 0.16807
## as.factor(AcidIndex)2.02271372429848 0.04586 *
## as.factor(AcidIndex)2.37629509167962 0.04424 *
## as.factor(AcidIndex)2.67051656830802 0.04375 *
## as.factor(AcidIndex)2.9188445277671 0.07168 .
## as.factor(AcidIndex)3.13100139587667 0.43317
## as.factor(AcidIndex)3.31417429494859 0.06293 .
## as.factor(AcidIndex)3.47378568897179 0.03304 *
## as.factor(STARS)-0.42623524866846 < 0.0000000000000002 ***
## as.factor(STARS)0.416552574962037 < 0.0000000000000002 ***
## as.factor(STARS)1.25934039859254 < 0.0000000000000002 ***
## as.factor(STARS)2.10212822222303 < 0.0000000000000002 ***
##
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.302 on 12762 degrees of freedom
## Multiple R-squared: 0.5441, Adjusted R-squared: 0.5429
## F-statistic: 475.9 on 32 and 12762 DF, p-value: < 0.0000000000000022

```

```

##          RMSE      Rsquared       MAE        aic        bic
## 1.2903542  0.5466928 1.0092020 43106.3022739 43359.8338054

```

Linear Model 6

For the final Linear Model, we leverage `stepAIC` on our Linear Model #5 to choose the most important features.

```

##
## Call:
## lm(formula = TARGET ~ VolatileAcidity + Chlorides + FreeSulfurDioxide +
##     TotalSulfurDioxide + Density + pH + Sulphates + Alcohol +
##     as.factor(LabelAppeal) + as.factor(AcidIndex) + as.factor(STARS),
##     data = clean_df)
##
## Residuals:
##    Min      1Q  Median      3Q      Max
## -4.9616 -0.8590  0.0352  0.8399  6.0675
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)               0.99019   0.75488  1.312
## VolatileAcidity          -0.07393   0.01156 -6.394
## Chlorides                 -0.03864   0.01177 -3.282
## FreeSulfurDioxide         0.04009   0.01178  3.403
## TotalSulfurDioxide        0.04960   0.01181  4.200
## Density                  -0.02270   0.01154 -1.967
## pH                        -0.01862   0.01170 -1.591
## Sulphates                -0.02837   0.01201 -2.362
## Alcohol                   0.05100   0.01183  4.313
## as.factor(LabelAppeal)-1.11204793733397 0.36722   0.06272  5.854
## as.factor(LabelAppeal)0.0101741115806247 0.83483   0.06116 13.649
## as.factor(LabelAppeal)1.13239616049522  1.30161   0.06391 20.367
## as.factor(LabelAppeal)2.25461820940981  1.88998   0.08416 22.456
## as.factor(AcidIndex)-3.59682937695875 -0.33511   0.76744 -0.437
## as.factor(AcidIndex)-1.79176983045029 -0.21824   0.75353 -0.290
## as.factor(AcidIndex)-0.545318540973785 -0.31837   0.75287 -0.423
## as.factor(AcidIndex)0.362910765511677 -0.42442   0.75293 -0.564
## as.factor(AcidIndex)1.05172974217783 -0.72561   0.75343 -0.963
## as.factor(AcidIndex)1.59059728918163 -1.03390   0.75463 -1.370
## as.factor(AcidIndex)2.02271372429848 -1.50407   0.75695 -1.987
## as.factor(AcidIndex)2.37629509167962 -1.52217   0.76131 -1.999
## as.factor(AcidIndex)2.67051656830802 -1.54018   0.76867 -2.004
## as.factor(AcidIndex)2.9188445277671 -1.38512   0.77635 -1.784
## as.factor(AcidIndex)3.13100139587667 -0.67937   0.88243 -0.770
## as.factor(AcidIndex)3.31417429494859 -1.75343   0.95178 -1.842
## as.factor(AcidIndex)3.47378568897179 -1.89498   0.89978 -2.106
## as.factor(STARS)-0.42623524866846  1.34682   0.03291 40.918
## as.factor(STARS)0.416552574962037  2.38256   0.03201 74.442
## as.factor(STARS)1.25934039859254  2.94276   0.03707 79.374
## as.factor(STARS)2.10212822222303  3.63105   0.05914 61.397
##
## (Intercept)                         Pr(>|t|)
##                                     0.189639

```

```

## VolatileAcidity          0.000000000167 ***
## Chlorides                 0.001034 **
## FreeSulfurDioxide         0.000669 ***
## TotalSulfurDioxide        0.000026926678 ***
## Density                   0.049224 *
## pH                        0.111585
## Sulphates                0.018191 *
## Alcohol                   0.000016245384 ***
## as.factor(LabelAppeal)-1.11204793733397 0.000000004904 ***
## as.factor(LabelAppeal)0.0101741115806247 < 0.0000000000000002 ***
## as.factor(LabelAppeal)1.13239616049522 < 0.0000000000000002 ***
## as.factor(LabelAppeal)2.25461820940981 < 0.0000000000000002 ***
## as.factor(AcidIndex)-3.59682937695875   0.662366
## as.factor(AcidIndex)-1.79176983045029   0.772104
## as.factor(AcidIndex)-0.545318540973785  0.672396
## as.factor(AcidIndex)0.362910765511677   0.572976
## as.factor(AcidIndex)1.05172974217783   0.335525
## as.factor(AcidIndex)1.59059728918163   0.170687
## as.factor(AcidIndex)2.02271372429848   0.046941 *
## as.factor(AcidIndex)2.37629509167962   0.045584 *
## as.factor(AcidIndex)2.67051656830802   0.045124 *
## as.factor(AcidIndex)2.9188445277671   0.074426 .
## as.factor(AcidIndex)3.13100139587667   0.441383
## as.factor(AcidIndex)3.31417429494859   0.065461 .
## as.factor(AcidIndex)3.47378568897179   0.035220 *
## as.factor(STARS)-0.42623524866846 < 0.0000000000000002 ***
## as.factor(STARS)0.416552574962037 < 0.0000000000000002 ***
## as.factor(STARS)1.25934039859254 < 0.0000000000000002 ***
## as.factor(STARS)2.10212822222303 < 0.0000000000000002 ***

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.302 on 12765 degrees of freedom
## Multiple R-squared:  0.544,  Adjusted R-squared:  0.543
## F-statistic: 525.1 on 29 and 12765 DF,  p-value: < 0.0000000000000022

##           RMSE      Rsquared       MAE       aic       bic
##     1.2904494  0.5466259  1.0093178 43102.1597330 43333.3208352

```

4. Model Selection & Analysis

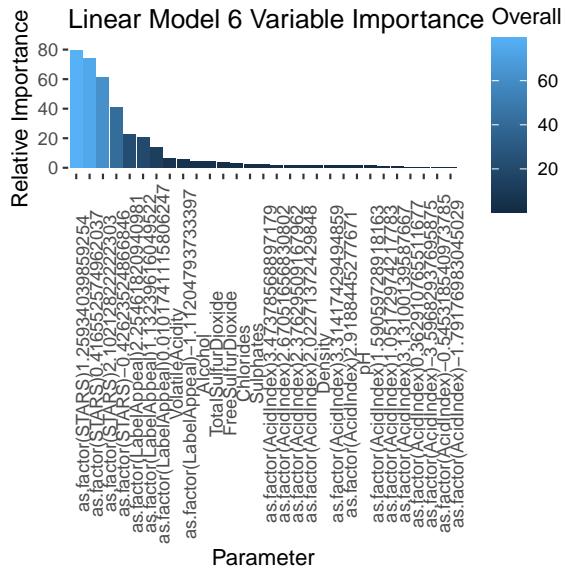
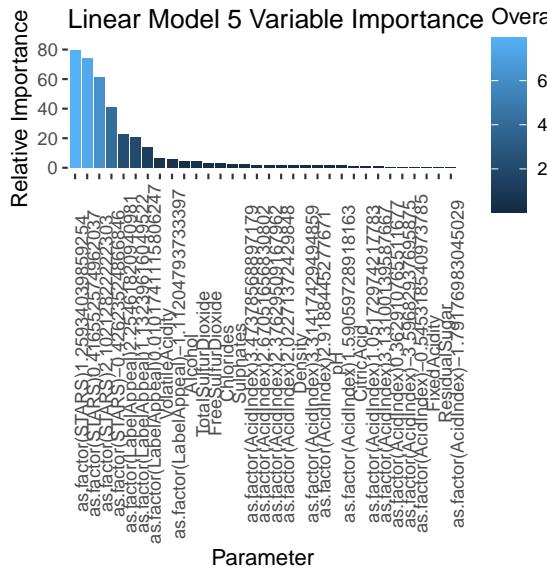
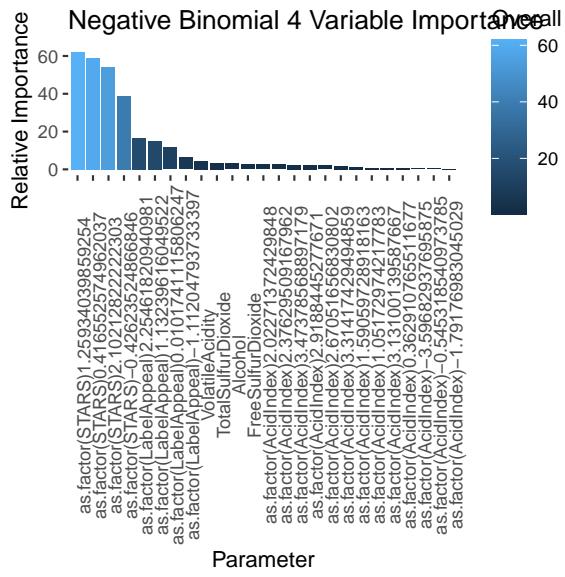
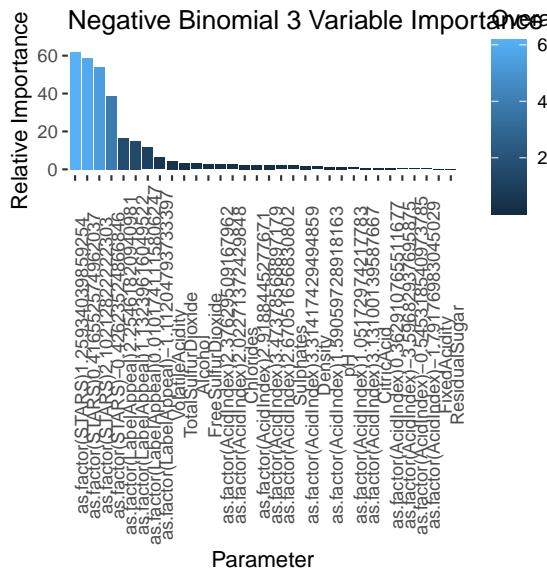
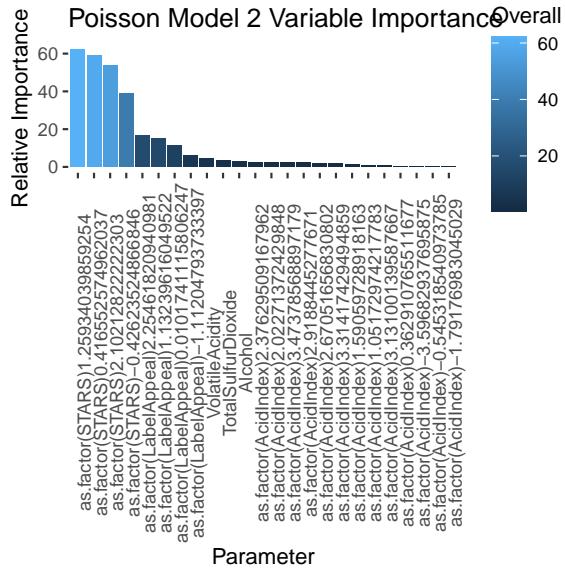
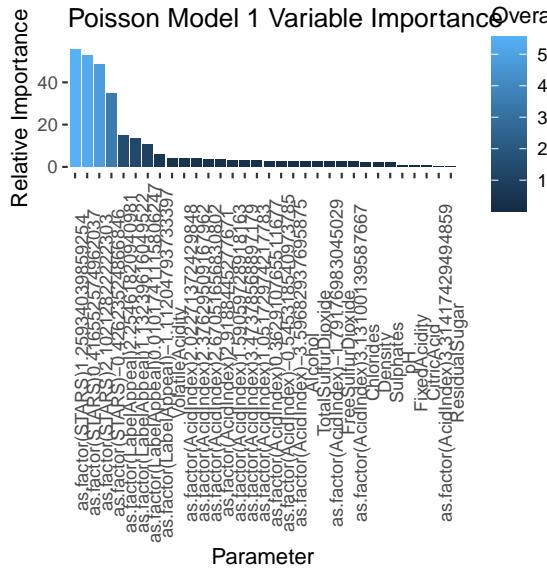
This table summarizes the **RMSE**, R^2 , **MAE**, **AIC** and **BIC** for all 6 models. In terms of raw metrics, The Linear regressions (**Linear Model 5** and **Linear Model 6**) had the overall best performance based on **RMSE** and R^2 ; however, **Poisson Model 1** had the best performance based on **AIC** and **BIC**.

Overall, **RMSE** an R^2 were not largely different across the 6 models, given this we chose **Poisson Model 1** as our final model since it had a far lower **AIC**.

	RMSE	Rsquared	MAE	aic	bic
poiss1_eval	2.592189	0.4659337	2.225719	36337.43	36576.15
poiss2_eval	2.585044	0.5228423	2.224620	45542.32	45728.74
nb3_eval	2.584713	0.5244026	2.224213	45540.13	45793.66
nb4_eval	2.584925	0.5233392	2.224534	45540.18	45741.51
lm5_eval	1.290354	0.5466928	1.009202	43106.30	43359.83
lm6_eval	1.290449	0.5466259	1.009318	43102.16	43333.32

The final thing we will take a look at is our variable importance for each model.

The final figure presented below shows the feature importance in each model. As we see, all 6 models identified the same top 10 features.



Predictions

We apply **Poisson Model #1** to the holdout evaluation set to predict the TARGET for these instances. We have saved these predictions as csv in the file `eval_predictions.csv`.

Source code: https://github.com/djlofland/DS621_F2020_Group3/tree/master/Homework_5/eval_predictions.csv

```
##           TARGET FixedAcidity VolatileAcidity CitricAcid ResidualSugar
## 1  0.17495342 -0.26524401   -1.51030924 -0.04455813   -0.4776009
## 2  1.35921746  0.84276407    0.07767213 -1.23934313   -0.7442725
## 3  0.93058461  0.01967235    1.81871194 -0.16055667   -1.1383538
## 4  0.85070705 -0.13861451   -0.28584168  1.73021959   -0.1309278
## 5 -0.01877411  0.68447720   -0.14553811 -0.03295827   -0.1250018
## 6  1.71061254  1.66585579   -0.36237090 -1.69173745   -0.1190758
##           Chlorides FreeSulfurDioxide TotalSulfurDioxide Density          pH
## 1  0.11673887      -0.05275591     1.19564455 -0.3402128  2.66647966
## 2  3.49856180      -0.45621338    -0.22730155 -0.1442311  0.23889195
## 3  0.03195779      -0.14689598    -0.19280589  1.9789246  2.06326090
## 4 -0.73421194      0.49191169    -0.13675044 -0.2085894 -0.01122314
## 5 -0.05282329      0.26328578    -0.29198092  1.3139028 -0.98225823
## 6  1.50777652      -1.88848742    0.08315942 -1.6483055 -0.21720028
##           Sulphates Alcohol LabelAppeal AcidIndex          STARS
## 1  0.1211079  0.4857435 -1.11204794 -1.7917698 -1.2690231
## 2  0.6038736  1.4782809  0.01017411 -1.7917698  0.4165526
## 3  0.1640204 -0.5202067  0.01017411  0.3629108 -0.4262352
## 4  1.6981424  0.4857435 -1.11204794  0.3629108 -0.4262352
## 5 -0.6405890 -1.5261568  0.01017411  1.5905973 -1.2690231
## 6 -0.5869484  0.2443154  1.13239616  0.3629108  2.1021282
```

References

- A Modern Approach to Regression with R: Simon Sheather
- Linear Models with R: Julian Faraway.
- R package vignette, mixtools: An R Package for Analyzing Finite Mixture Models
- 7 Classic OLS assumptions
- Detecting Multicollinearity with VIF

Appendix

R Code

```
# =====
# Load Libraries and Define Helper functions
# =====

library(MASS)
library(rpart.plot)
library(ggplot2)
library(ggfortify)
library(gridExtra)
library(forecast)
library(fpp2)
```

```

library(fma)
library(kableExtra)
library(e1071)
library(mlbench)
library(ggcorrplot)
library(DataExplorer)
library(timeDate)
library(caret)
library(GGally)
library(corrplot)
library(RColorBrewer)
library(tibble)
library(tidyr)
library(tidyverse)
library(dplyr)
library(reshape2)
library(mixtools)
library(tidymodels)
library(ggpmisc)
library(regclass)
library(skimr)

#' Print a side-by-side Histogram and QQPlot of Residuals
#'
#' @param model A model
#' @examples
#' residPlot(myModel)
#' @return null
#' @export
residPlot <- function(model) {
  # Make sure a model was passed
  if (is.null(model)) {
    return
  }

  layout(matrix(c(1,1,2,3), 2, 2, byrow = TRUE))
  plot(residuals(model))
  hist(model[["residuals"]], freq = FALSE, breaks = "fd", main = "Residual Histogram",
       xlab = "Residuals", col="lightgreen")
  lines(density(model[["residuals"]]), kernel = "ep", col="blue", lwd=3)
  curve(dnorm(x,mean=mean(model[["residuals"]])), sd=sd(model[["residuals"]]), col="red", lwd=3, lty="dashed")
  qqnorm(model[["residuals"]], main = "Residual Q-Q plot")
  qqline(model[["residuals"]], col="red", lwd=3, lty="dotted")
  par(mfrow = c(1, 1))
}

#' Print a Variable Importance Plot for the provided model
#'
#' @param model The model
#' @param chart_title The Title to show on the plot
#' @examples
#' variableImportancePlot(myLinearModel, 'My Title')
#' @return null
#' @export
variableImportancePlot <- function(model=NULL, chart_title='Variable Importance Plot') {

```

```

# Make sure a model was passed
if (is.null(model)) {
  return
}

# use caret and ggplot to print a variable importance plot
varImp(model) %>% as.data.frame() %>%
  ggplot(aes(x = reorder(rownames(.), desc(Overall)), y = Overall)) +
  geom_col(aes(fill = Overall)) +
  theme(panel.background = element_blank(),
        panel.grid = element_blank(),
        axis.text.x = element_text(angle = 90)) +
  scale_fill_gradient() +
  labs(title = chart_title,
       x = "Parameter",
       y = "Relative Importance")
}

#' Print a Facet Chart of histograms
#'
#' @param df Dataset
#' @param box Facet size (rows)
#' @examples
#' histbox(my_df, 3)
#' @return null
#' @export
histbox <- function(df, box) {
  par(mfrow = box)
  ndf <- dimnames(df)[[2]]

  for (i in seq_along(ndf)) {
    data <- na.omit(unlist(df[, i]))
    hist(data, breaks = "fd", main = paste("Histogram of", ndf[i]),
          xlab = ndf[i], freq = FALSE)
    lines(density(data, kernel = "ep"), col = 'red')
  }

  par(mfrow = c(1, 1))
}

#' Extract key performance results from a model
#'
#' @param model A linear model of interest
#' @examples
#' model_performance_extraction(my_model)
#' @return data.frame
#' @export
model_performance_extraction <- function(model=NULL) {
  # Make sure a model was passed
  if (is.null(model)) {
    return
  }

  data.frame("RSE" = model$sigma,
            "Adj R2" = model$adj.r.squared,
            "F-Statistic" = model$fstatistic[1])
}

```

```

}

# =====
# Load Data set
# =====

# Load Wine dataset
df <- read.csv('https://raw.githubusercontent.com/djlofland/DS621_F2020_Group3/master/Homework_5/dataset_wine.csv')
df_eval <- read.csv('https://raw.githubusercontent.com/djlofland/DS621_F2020_Group3/master/Homework_5/dataset_wine_eval.csv')

# =====
# Summary Stats
# =====

# Display summary statistics
summary(df)

# =====
# Distributions
# =====

# Prepare data for ggplot
gather_df <- df %>%
  gather(key = 'variable', value = 'value')

# Histogram plots of each variable
ggplot(gather_df) +
  geom_histogram(aes(x=value, y = ..density..), bins=30) +
  geom_density(aes(x=value), color='blue') +
  facet_wrap(. ~variable, scales='free', ncol=4)

# =====
# Boxplots
# =====

# Prepare data for ggplot
gather_df <- df %>%
  gather(key = 'variable', value = 'value')

# Boxplots for each variable
ggplot(gather_df, aes(variable, value)) +
  geom_boxplot() +
  facet_wrap(. ~variable, scales='free', ncol=6)

df_character_wide <- df %>%
  select(TARGET, STARS, LabelAppeal, AcidIndex) %>%
  pivot_longer(cols = -TARGET, names_to="variable", values_to="value") %>%
  arrange(variable, value)

df_character_wide %>%
  ggplot(mapping = aes(x = factor(value), y = TARGET)) +
  geom_boxplot() +
  facet_wrap(~variable, scales="free") +
  theme_bw()

```

```

    theme(axis.text.x = element_text(angle = 90))

# =====
# Variable Plots
# =====

# Plot scatter plots of each variable versus the target variable
featurePlot(df[,2:ncol(df)], df[,1], pch = 20)

# =====
# Missing Data
# =====

# Identify missing data by Feature and display percent breakout
missing <- colSums(df %>% sapply(is.na))
missing_pct <- round(missing / nrow(df) * 100, 2)
stack(sort(missing_pct, decreasing = TRUE))

# separate our features from target so we don't inadvertently transform the target
training_x <- df %>% select(-TARGET)
training_y <- df$TARGET

# separate our features from target so we don't inadvertently transform the target
eval_x <- df_eval %>% select(-TARGET)
eval_y <- df_eval$TARGET

create_na_dummy <- function(vector) {
  as.integer(vector %>% is.na())
}

impute_missing <- function(data) {
  # Replace missing STARS with 0
  data$STARS <- data$STARS %>%
    replace_na(0)

  return(data)
}

# Replace missing STARS with 'unknown' and convert STASR to a factor
training_x <- impute_missing(training_x)
eval_x <- impute_missing(eval_x)

imputation <- preProcess(training_x, method = c("knnImpute", 'BoxCox'))
# summary(imputation)

training_x_imp <- predict(imputation, training_x)
eval_x_imp <- predict(imputation, eval_x)

clean_df <- cbind(training_y, training_x_imp) %>%
  as.data.frame() %>%
  rename(TARGET = training_y)

clean_eval_df <- cbind(eval_y, eval_x_imp) %>%

```

```

as.data.frame() %>%
  rename(TARGET = eval_y)

# =====
# Feature-target correlations
# =====

# Show feature correlations/target by decreasing correlation
stack(sort(cor(clean_df[,1], clean_df[,2:ncol(clean_df)]), decreasing=TRUE))

# =====
# Multicollinearity
# =====

# Calculate and plot the Multicollinearity
correlation = cor(clean_df, use = 'pairwise.complete.obs')
corrplot(correlation, 'ellipse', type = 'lower', order = 'hclust',
         col=brewer.pal(n=8, name="RdYlBu"))

# =====
# Transform non-normal variables
# =====

# created empty data frame to store transformed variables
#df_temp <- data.frame(matrix(ncol = 1, nrow = length(clean_df$TARGET)))

# performed log transformation
#df_temp$Chlorides <- clean_df$Chlorides
#df_temp$Chlorides_transform <- log(clean_df$Chlorides)

# performed log transformation
#df_temp$CitricAcid <- clean_df$CitricAcid
#df_temp$CitricAcid_transform <- log(clean_df$CitricAcid)

# performed a log transformation
#df_temp$FixedAcidity <- clean_df$FixedAcidity
#df_temp$FixedAcidity_transform <- log(clean_df$FixedAcidity)
# performed a log transformation
#df_temp$FreeSulfurDioxide <- clean_df$FreeSulfurDioxide
#df_temp$FreeSulfurDioxide_transform <- log(clean_df$FreeSulfurDioxide)
# performed a log transformation
#df_temp$ResidualSugar <- clean_df$ResidualSugar
#df_temp$ResidualSugar_transform <- log(clean_df$ResidualSugar)
# performed a log transformation
#df_temp$Sulphates <- clean_df$Sulphates
#df_temp$Sulphates_transform <- log(clean_df$Sulphates)
# performed a log transformation
#df_temp$TotalSulfurDioxide <- clean_df$TotalSulfurDioxide
#df_temp$TotalSulfurDioxide_transform <- log(clean_df$TotalSulfurDioxide)
# performed a log transformation
#df_temp$VolatileAcidity <- clean_df$VolatileAcidity
#df_temp$VolatileAcidity_transform <- log(clean_df$VolatileAcidity)

```

```

# =====
# Finalizing dataset for model building
# =====

options(scipen = 999)

#75% data test training split
# get training/test split
y_raw <- as.matrix(clean_df$TARGET)
trainingRows <- createDataPartition(y_raw, p=0.8, list=FALSE)

# Build training data sets
trainX <- clean_df[trainingRows, ] %>% select(-TARGET)
trainY <- clean_df[trainingRows, ] %>% select(TARGET)

# put remaining rows into the test sets
testX <- clean_df[-trainingRows, ] %>% select(-TARGET)
testY <- clean_df[-trainingRows, ] %>% select(TARGET)

# Build a DF
trainingData <- as.data.frame(trainX)
trainingData$TARGET <- trainY$TARGET
print(paste('Number of Training Samples: ', dim(trainingData)[1]))

testingData <- as.data.frame(testX)
testingData$TARGET <- testY$TARGET
print(paste('Number of Testing Samples: ', dim(testingData)[1]))

model_test_perf <- function(model, trainX, trainY, testX, testY) {
  # Evaluate Model 1 with testing data set
  predictedY <- predict(model, newdata=trainX)

  model_results <- data.frame(obs = trainY, pred=predictedY)
  colnames(model_results) = c('obs', 'pred')

  # This grabs RMSE, Rsquaredand MAE by default
  model_eval <- defaultSummary(model_results)

  # Add AIC score to the results
  if ('aic' %in% model) {
    model_eval[4] <- model$aic
  } else {
    model_eval[4] <- AIC(model)
  }

  names(model_eval)[4] <- 'aic'

  # Add BIC score to the results
  model_eval[5] <- BIC(model)
  names(model_eval)[5] <- 'bic'

}

return(model_eval)

```

```

# =====
# Poisson Model 1
# =====

options(scipen = 999)

poiss1 <- glm(TARGET ~ FixedAcidity + VolatileAcidity + CitricAcid + ResidualSugar +
Chlorides + FreeSulfurDioxide + TotalSulfurDioxide + Density +
pH + Sulphates + Alcohol +
as.factor(LabelAppeal) +
as.factor(AcidIndex) +
as.factor(STARS),
data=trainingData,
family=poisson)

summary(poiss1)

# Evaluate Model 1 with testing data set
(poiss1_eval <- model_test_perf(poiss1, trainX, trainY, testX, testY))
po1VIP <- variableImportancePlot(poiss1, "Poisson Model 1 Variable Importance")

# =====
# Poisson Model 2
# =====

poiss2 <- glm(TARGET ~ VolatileAcidity + TotalSulfurDioxide + Alcohol +
as.factor(LabelAppeal) +
as.factor(AcidIndex) +
as.factor(STARS),
data=clean_df,
family=poisson)

summary(poiss2)

# Evaluate Model 1 with testing data set
(poiss2_eval <- model_test_perf(poiss2, trainX, trainY, testX, testY))
po2VIP <- variableImportancePlot(poiss2, "Poisson Model 2 Variable Importance")

# =====
# Negative Binomial Model 3
# =====

nb3 <- glm.nb(TARGET ~ FixedAcidity + VolatileAcidity + CitricAcid + ResidualSugar +
Chlorides + FreeSulfurDioxide + TotalSulfurDioxide + Density +
pH + Sulphates + Alcohol +
as.factor(LabelAppeal) +
as.factor(AcidIndex) +
as.factor(STARS),
data=clean_df)
summary(nb3)

```

```

# Evaluate Model 1 with testing data set
(nb3_eval <- model_test_perf(nb3, trainX, trainY, testX, testY))
nb3VIP <- variableImportancePlot(nb3, "Negative Binomial 3 Variable Importance") (model3$fit, "Linear Model 3 Variable Importance")

# =====
# Negative Binomial Model 4
# =====

nb4 <- glm.nb(TARGET~ VolatileAcidity + FreeSulfurDioxide + TotalSulfurDioxide + Alcohol +
               as.factor(LabelAppeal) +
               as.factor(AcidIndex) +
               as.factor(STARS),
               data=clean_df)

summary (nb4)

# Evaluate Model 1 with testing data set
(nb4_eval <- model_test_perf(nb4, trainX, trainY, testX, testY))
nb4VIP <- variableImportancePlot(nb4, "Negative Binomial 4 Variable Importance") (model4$fit, "Linear Model 4 Variable Importance")

# =====
# Linear Model 5
# =====

lm5 <- lm(TARGET ~ FixedAcidity + VolatileAcidity + CitricAcid + ResidualSugar +
           Chlorides + FreeSulfurDioxide + TotalSulfurDioxide + Density +
           pH + Sulphates + Alcohol +
           as.factor(LabelAppeal) +
           as.factor(AcidIndex) +
           as.factor(STARS),
           data=clean_df)

summary(lm5)

# Evaluate Model 1 with testing data set
(lm5_eval <- model_test_perf(lm5, trainX, trainY, testX, testY))
lm5VIP <- variableImportancePlot(lm5, "Linear Model 5 Variable Importance") (model5$fit, "Linear Model 5 Variable Importance")

# =====
# Linear Model 6
# =====

lm6 <- stepAIC(lm5, direction = "both",
                scope = list(upper = lm5, lower = ~ 1),
                scale = 0, trace = FALSE)

summary(lm6)

# Evaluate Model 1 with testing data set
(lm6_eval <- model_test_perf(lm6, trainX, trainY, testX, testY))

lm6VIP <- variableImportancePlot(lm6, "Linear Model 6 Variable Importance")

```

```

# =====
# Model selection and analysis
# =====

models_summary <- rbind(poiss1_eval, poiss2_eval, nb3_eval, nb4_eval, lm5_eval, lm6_eval)

kable(models_summary) %>%
  kable_styling(bootstrap_options = "basic", position = "center")

grid.arrange(po1VIP, po2VIP, nb3VIP, nb4VIP, lm5VIP, lm6VIP, ncol = 2)

# =====
Predictions
# =====

eval_data <- clean_eval_df %>% select(-TARGET)

predictions <- predict(poiss1, eval_data)
clean_eval_df$TARGET <- predictions

write.csv(clean_eval_df, 'eval_predictions.csv', row.names=F)

head(clean_eval_df)

# =====
End of R Code
# =====

```